Amendments to the Specification:

Please replace the paragraph beginning on page 16, line 28, with the following rewritten paragraph:

~~Figure 4 represents a~~ Figures 4A-C represent phylogenetic analysis identifying the HERV-W ~~family~~family; Figure 4A represents a phylogenetic analysis carried out on the nucleic acids in the LTR region; Figure 4B represents a phylogenetic analysis carried out on the nucleic acids in the POL region; Figure 4C represents a phylogenetic analysis carried out in the ENV region.

Please replace the paragraph beginning on page 16, line 30, with the following rewritten paragraph:

~~Figure 5 represents~~ Figures 5A and B represent the alignment of the 5' and 3' flanking regions of the clone RG083M05 [SEQ ID NO: 43 (5-RG-28000-28872) and SEQ ID NO: 44 (3-RG-37500-38314)] with the terminal 5' and/or 3' regions of some placental clones [SEQ ID NO: 45 (3-PH74.2358-2782), SEQ ID NO: 46 (3-C4C5.710-1136), SEQ ID NO: 47 (5-6A2.1-600), SEQ ID NO: 48 (5-PH74.1-530) and SEQ ID NO: 49 (5-24.4.1-486)]; the CAAC tandem flanking the 3' and 5' LTRs is doubly underlined under the DNA sequences, the consensus LTR sequence of 783 bp (base pairs) (SEQ ID NO: 15) is indicated under the alignment; the PPT upstream of the 5' end of LTR and the PBS downstream of the 3' end of LTR are indicated; the U3R and U5 regions are indicated; the sites corresponding to the binding of the transcription factor are underlined and numbered from 1 to 6; the region -73 to 284 corresponds to the sequence evaluated in "CAT assay"; * corresponds to putative sites for "capping"; [polyA] indicates the polyadenylation signal.

Please replace the paragraph beginning on page 21, line 12, with the following rewritten paragraph:

A phylogenetic analysis was carried out at the level of the nucleic acids on 11 different subregions of the reconstructed genomic RNA, and at the protein level on 2 different subregions of env. All the trees obtained exhibit the same topology regardless of the region studied. This is illustrated in ~~Figure 4~~ Figures 4A and 4B at the level of the nucleic acids in the most conserved LTR and pol ~~regions~~ regions, respectively, between the sequences obtained and ERV-9 and RTLV-H. The trees clearly show that the experimental sequences describe a new family distinct from ERV-9 and very distinct from RTLV-H as underlined by the "bootstrap" analysis. These sequences are found on several chromosomes, in particular chromosomes 5, 7, 14, 16, 21, 22 and X with a high apparent concentration of LTR on the X chromosome.

Please replace the paragraph beginning on page 21, line 35, with the following rewritten paragraph:

The reconstructed sequence (RNA) is integrally contained inside the genomic clone RG083M05 (9.6 Kb) and exhibits a 96% similarity with two discontinuous regions of this clone which also contains repeat regions at each end. The alignment of the experimental sequences corresponding to the 5' and 3' regions of the genomic RNA reconstructed with the DNA of the clone RG083M05 [5' (5-RG-28000-28872) (SEQ ID NO: 43) and 3' (3-RG-37500-38314) (SEQ ID NO: 44)] made it possible to deduce an LTR sequence and to identify elements characteristic of the retroviruses, in particular those involved in the reverse transcription, namely PBS downstream of the 5' LTR and the PPT upstream of the 3' LTR ~~(cf Figure 5).~~ (cf Figures 5A and B). It is observed that the U3 element is extremely short in comparison with that observed in the mammalian type C retroviruses, and is

comparable in size to the U3 region generally described in the type D retroviruses and the avian retroviruses. The region corresponding to bases 2364 to 2720 of the clone cl.PH74 (SEQ ID NO: 7) was amplified by PCR and subcloned into the vector pCAT3 (Promega) in order to carry out the evaluation of the promoter activity. A significant activity was found in HeLa cells by the so-called "CAT assay" method showing the functionality of the promoter sequence of the LTR.